

SEQUENCE LISTING

<110> Sims, John E.
Smith, Dirk E.

<120> IL-1 RECEPTOR ACCESSORY PROTEIN

<130> 3151-A

<140> --to be assigned--

<141> 2001-10-26

<150> US 60/244,831

<151> 2000-10-31

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 2064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2064)

<223>

<220>

<221> misc_feature

<222> (1792)..(1792)

<223> "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.

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caa agt gat gcc tca gaa cgc tgc gat gac tgg gga cta gac acc atg	96
Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met	
20 25 30	
agg caa atc caa gtg ttt gaa gat gag cca gct cgc atc aag tgc cca	144
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro	
35 40 45	
ctc ttt gaa cac ttc ttg aaa ttc aac tac agc aca gcc cat tca gct	192
Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala	
50 55 60	
ggc ctt act ctg atc tgg tat tgg act agg cag gac cgg gac ctt gag	240
Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu	
65 70 75 80	
gag cca att aac ttc cgc ctc ccc gag aac cgc att agt aag gag aaa	288
Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys	
85 90 95	

10051727-1005001

gat gtg ctg tgg ttc cgg ccc act ctc ctc aat gac act ggc aac tat 336
Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
100 105 110

acc tgc atg tta agg aac act aca tat tgc agc aaa gtt gca ttt ccc 384
Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
115 120 125

ttg gaa gtt gtt caa aaa gac agc tgt ttc aat tcc ccc atg aaa ctc 432
Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
130 135 140

cca gtg cat aaa ctg tat ata gaa tat ggc att cag agg atc act tgt 480
Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145 150 155 160

cca aat gta gat gga tat ttt cct tcc agt gtc aaa ccg act atc act 528
Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
165 170 175

tgg tat atg ggc tgt tat aaa ata cag aat ttt aat aat gta ata ccc 576
Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
180 185 190

gaa ggt atg aac ttg agt ttc ctc att gcc tta att tca aat aat gga 624
Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
195 200 205

aat tac aca tgt gtt gtt aca tat cca gaa aat gga cgt acg ttt cat 672
Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
210 215 220

ctc acc agg act ctg act gta aag gta gta ggc tct cca aaa aat gca 720
Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
225 230 235 240

gtg ccc cct gtg atc cat tca cct aat gat cat gtg gtc tat gag aaa 768
Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
245 250 255

gaa cca gga gag gag cta ctc att ccc tgt acg gtc tat ttt agt ttt 816
Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
260 265 270

ctg atg gat tct cgc aat gag gtt tgg tgg acc att gat gga aaa aaa 864
Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
275 280 285

cct gat gac atc act att gat gtc acc att aac gaa agt ata agt cat 912
Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
290 295 300

agt aga aca gaa gat gaa aca aga act cag att ttg agc atc aag aaa 960
Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305 310 315 320

gtt acc tct gag gat ctc aag cgc agc tat gtc tgt cat gct aga agt 1008
Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
325 330 335

10061727-100601

gcc aaa ggc gaa gtt gcc aaa gca gcc aag gtg aag cag aaa gtg cca 1056
 Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
 340 345 350

gct cca aga tac aca gtg gaa ctg gct tgt ggt ttt gga gcc aca gtc 1104
 Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
 355 360 365

ctg cta gtg gtg att ctc att gtt gtt tac cat gtt tac tgg cta gag 1152
 Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
 370 375 380

atg gtc cta ttt tac cgg gct cat ttt gga aca gat gaa acc att tta 1200
 Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
 385 390 395 400

gat gga aaa gag tat gat att tat gta tcc tat gca agg aat gcg gaa 1248
 Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
 405 410 415

gaa gaa gaa ttt gta tta ctg acc ctc cgt gga gtt ttg gag aat gaa 1296
 Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
 420 425 430

ttt gga tac aag ctg tgc atc ttt gac cga gac agt ctg cct ggg gga 1344
 Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
 435 440 445

aat aca gtg gaa gca gtt ttt gat ttc att cag aga agc aga agg atg 1392
 Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
 450 455 460

att gtt gtt ctg agc cct gac tat gtg aca gaa aag agc atc agc atg 1440
 Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
 465 470 475 480

ctg gag ttt aaa ctg ggt gtc atg tgc cag aac tcc att gcc acc aag 1488
 Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
 485 490 495

ctc att gtg gtt gag tac cgt ccc ctt gag cac ccg cac cca ggc att 1536
 Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
 500 505 510

ctt cag ctc aaa gag tct gtg tct ttt gtg agc tgg aag gga gaa aag 1584
 Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
 515 520 525

tcc aaa cat tct ggc tct aaa ttc tgg aaa gct ttg cgg ttg gct ctt 1632
 Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
 530 535 540

ccc ctg aga agt ctg agt gcc agt tct ggc tgg aat gag agc tgc tct 1680
 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
 545 550 555 560

tcc cag tct gac atc agt ctg gat cac gtt caa agg agg aga agt cgt 1728
 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
 565 570 575

ttg aaa gag ccc cca gaa ctt cag agc tca gag agg gct gca ggt agc 1776
 Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
 580 585 590

cct cca gcc cca ggc nca atg tcc aag cac cga ggg aag tcc tcc gcc 1824
 Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
 595 600 605

acc tgc cgc tgt tgt gtc acc tac tgt gaa gga gag aat cac ctt agg 1872
 Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
 610 615 620

aac aag agc cgg gca gag att cat aac cag ccc cag tgg gag aca cac 1920
 Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His
 625 630 635 640

ctc tgt aag cct gtt ccc caa gag tca gaa act caa tgg ata caa aat 1968
 Leu Cys Lys Pro Val Pro Gln Glu Ser Glu Thr Gln Trp Ile Gln Asn
 645 650 655

ggc acc aga ttg gaa ccc cct gct ccc cag atc tca gcc ctt gct ctt 2016
 Gly Thr Arg Leu Glu Pro Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu
 660 665 670

cat cat ttc acg gac tta tcc aat aac aac gac ttt tat atc cta taa 2064
 His His Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
 675 680 685

<210> 2

<211> 687

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (598)..(598)

<223> The 'Xaa' at location 598 stands for Thr or Pro.

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Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
 20 25 30

Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
 35 40 45

Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
 50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
 65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
130 135 140

Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
165 170 175

Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
180 185 190

Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
195 200 205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
210 215 220

Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
225 230 235 240

Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
245 250 255

Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
260 265 270

Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
275 280 285

Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
290 295 300

Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305 310 315 320

Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
325 330 335

Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
340 345 350

Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
355 360 365

Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
370 375 380

Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
385 390 395 400

Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
405 410 415

Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
420 425 430

Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
435 440 445

Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
450 455 460

Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
465 470 475 480

Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
485 490 495

Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
500 505 510

Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
515 520 525

Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
530 535 540

Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
545 550 555 560

10061727-102604

Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
565 570 575

Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
580 585 590

Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
595 600 605

Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
610 615 620

Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His
625 630 635 640

Leu Cys Lys Pro Val Pro Gln Glu Ser Glu Thr Gln Trp Ile Gln Asn
645 650 655

Gly Thr Arg Leu Glu Pro Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu
660 665 670

His His Phe Thr Asp Leu Ser Asn Asn Asp Phe Tyr Ile Leu
675 680 685

<210> 3
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<220>
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<222> (1)..(2058)
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cag agt cat gct tcg gag cgc tgt gat gac tgg gga cta gat acc atg 96
Gln Ser His Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
20 25 30
cga caa atc caa gtg ttt gaa gat gag ccg gct cga atc aag tgc ccc 144
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
35 40 45
ctc ttt gaa cac ttc ctg aag tac aac tac agc act gcc cat tcc tct 192
Leu Phe Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser
50 55 60

ggc ctt acc ctg atc tgg tac tgg acc agg caa gac cgg gac ctg gag 240
 Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
 65 70 75 80

gag ccc att aac ttc cgc ctc cca gag aat cgc atc agt aag gag aaa 288
 Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
 85 90 95

gat gtg ctc tgg ttc cgg ccc acc ctc ctc aat gac acg ggc aat tac 336
 Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
 100 105 110

acc tgc atg ttg agg aac aca act tac tgc agc aaa gtt gca ttt ccc 384
 Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
 115 120 125

ctg gaa gtt gtt cag aag gac agc tgt ttc aat tct gcc atg aga ttc 432
 Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe
 130 135 140

cca gtg cac aag atg tat att gaa cat ggc att cat aag atc aca tgt 480
 Pro Val His Lys Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys
 145 150 155 160

cca aat gta gac gga tac ttt cct tcc agt gtc aaa cca tcg gtc act 528
 Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr
 165 170 175

tgg tat aag ggt tgt act gaa ata gtg gac ttt cat aat gta cta ccc 576
 Trp Tyr Lys Gly Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro
 180 185 190

gag ggc atg aac ttg agc ttt ttc atc ccc ttg gtt tca aat aac gga 624
 Glu Gly Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly
 195 200 205

aat tac aca tgt gtg gtt aca tat cct gaa aac gga cgt ctc ttt cac 672
 Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His
 210 215 220

ctc acc agg act gtg act gta aag gtg gtg ggc tca cca aag gat gca 720
 Leu Thr Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala
 225 230 235 240

ttg cca ccc cag atc tat tct cca aat gac cgt gtt gtc tat gag aaa 768
 Leu Pro Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys
 245 250 255

gaa cca gga gag gaa ctg gtt att ccc tgc aaa gtc tat ttc agt ttc 816
 Glu Pro Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe
 260 265 270

att atg gac tcc cac aat gag gtc tgg tgg acc att gat gga aag aag 864
 Ile Met Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
 275 280 285

cct gat gac gtc aca gtc gac atc act att aat gaa agt gta agt tat 912
 Pro Asp Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr
 290 295 300

10004707 10004707

tct tca acg gaa gat gaa aca agg act cag att ttg agc atc aag aaa Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys 305 310 315 320	960
gtc acc ccg gag gat ctc agg cgc aac tat gtc tgt cat gct cga aat Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn 325 330 335	1008
acc aaa ggg gaa gct gag cag gct gcc aag gtg aaa cag aaa gtc ata Thr Lys Gly Glu Ala Glu Gln Ala Lys Val Lys Gln Lys Val Ile 340 345 350	1056
cca cca agg tac aca gta gaa ctc gcc tgt ggt ttt gga gcc acg gtc Pro Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val 355 360 365	1104
ttt ctg gta gtg gtt ctc att gtg gtt tac cat gtt tac tgg ctg gag Phe Leu Val Val Val Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu 370 375 380	1152
atg gtc ctc ttt tac cga gct cac ttt gga aca gat gaa aca att ctt Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu 385 390 395 400	1200
gat gga aag gag tat gat att tat gtt tcc tat gca aga aat gtg gaa Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Val Glu 405 410 415	1248
gaa gag gaa ttt gtg ctg ctg acg ctg cgt gga gtt ttg gag aat gag Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu 420 425 430	1296
ttt gga tac aag ctg tgc atc ttc gac aga gac agc ctg cct ggg gga Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly 435 440 445	1344
aat acc gtg gaa gca gtt ttt gat ttc att cag agg agc cga agg atg Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met 450 455 460	1392
att gtt gtc ctg agc cct gac tat gtg aca gaa aag agc atc agc atg Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met 465 470 475 480	1440
ctg gag ttt aag ctg ggt gtc atg tgc cag aac tcc att gcc act aag Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys 485 490 495	1488
ctc att gtg gtg gag tac cgt ccg ctt gag caa ccc cat cca ggc atc Leu Ile Val Val Glu Tyr Arg Pro Leu Glu Gln Pro His Pro Gly Ile 500 505 510	1536
atg cag ctg aag gag tct gtg tct ttt gta agc tgg aag gga gaa aag Met Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys 515 520 525	1584
tcc aaa cat tct ggc tcc aag ttc tgg aag gcc ttg cgt ttg gct ctt Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu 530 535 540	1632

10061727.102664

ccc ctg aga agt ctg agc gcc agc tcc ggc tgg aat gag agc tgt tct 1680
 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
 545 550 555 560

tct cag tct gac atc agt ctg gat cat gtt cag agg aga agt cgt ttg 1728
 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Ser Arg Leu
 565 570 575

aaa gag ccc cca gaa ctc cga agc tca gag agg gtg tct gga gca gag 1776
 Lys Glu Pro Pro Glu Leu Arg Ser Ser Glu Arg Val Ser Gly Ala Glu
 580 585 590

cca gcc ccg ggc acg atg tcc aag cac cga ggg aaa ccc tca gca gcc 1824
 Pro Ala Pro Gly Thr Met Ser Lys His Arg Gly Lys Pro Ser Ala Ala
 595 600 605

tgt cgc tgc tgt gtc acc tac tgt gaa gga gaa agt cac ctc agg agc 1872
 Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Ser His Leu Arg Ser
 610 615 620

aag agc cgg gca gag atg cac acg cat ccc cag tgg gaa aca cac ctc 1920
 Lys Ser Arg Ala Glu Met His Thr His Pro Gln Trp Glu Thr His Leu
 625 630 635 640

tgt aag cct cct ctc caa gag tct gaa agt cag tgg ata caa aat ggc 1968
 Cys Lys Pro Pro Leu Gln Glu Ser Glu Ser Gln Trp Ile Gln Asn Gly
 645 650 655

acc cga ccc gaa ccc gct ccc cag atc tca gct ctt gca ctc cgc cac 2016
 Thr Arg Pro Glu Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu Arg His
 660 665 670

ttt aca gat tta tcc aat aac aat gac ttt tat atc cta taa 2058
 Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
 675 680 685

<210> 4
 <211> 685
 <212> PRT
 <213> Mus musculus

<400> 4

Met Gly Leu Leu Trp Tyr Leu Met Ser Leu Ser Phe Tyr Gly Ile Leu
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Gln Ser His Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
 20 25 30

Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
 35 40 45

Leu Phe Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser
 50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe
130 135 140

Pro Val His Lys Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr
165 170 175

Trp Tyr Lys Gly Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro
180 185 190

Glu Gly Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly
195 200 205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His
210 215 220

Leu Thr Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala
225 230 235 240

Leu Pro Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys
245 250 255

Glu Pro Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe
260 265 270

Ile Met Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
275 280 285

Pro Asp Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr
290 295 300

10061727-102501

Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305 310 315 320

Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn
325 330 335

Thr Lys Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys Val Ile
340 345 350

Pro Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
355 360 365

Phe Leu Val Val Val Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
370 375 380

Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
385 390 395 400

Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Val Glu
405 410 415

Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
420 425 430

Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
435 440 445

Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
450 455 460

Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
465 470 475 480

Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
485 490 495

Leu Ile Val Val Glu Tyr Arg Pro Leu Glu Gln Pro His Pro Gly Ile
500 505 510

Met Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
515 520 525

Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
530 535 540

10061727 102601

Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
545 550 555 560

Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Ser Arg Leu
565 570 575

Lys Glu Pro Pro Glu Leu Arg Ser Ser Glu Arg Val Ser Gly Ala Glu
580 585 590

Pro Ala Pro Gly Thr Met Ser Lys His Arg Gly Lys Pro Ser Ala Ala
595 600 605

Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Ser His Leu Arg Ser
610 615 620

Lys Ser Arg Ala Glu Met His Thr His Pro Gln Trp Glu Thr His Leu
625 630 635 640

Cys Lys Pro Pro Leu Gln Glu Ser Glu Ser Gln Trp Ile Gln Asn Gly
645 650 655

Thr Arg Pro Glu Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu Arg His
660 665 670

Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
675 680 685